

# SEQUENCE LISTING

<110> Sewalt, Vincent J. H.  
Jung, Rudolf  
Hu, Wang-Nan  
Meeley, Robert B.

<120> Improved Grain Quality Through Altered  
Expression of Seed Proteins

<130> 1276

<150> US 60/246,455

<151> 2000-11-07

<160> 10

<170> FastSEQ for Windows Version 3.0

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<213> Zea mays

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atg aag ctg gtg ctt gtg gtt ctt gct ttc att gct tta gta tca agt	167
Met Lys Leu Val Leu Val Val Leu Ala Phe Ile Ala Leu Val Ser Ser	
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Val Ser Cys Thr Gln Thr Gly Gly Cys Ser Cys Gly Gln Gln Ser	
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cat gag cag caa cat cat cca caa caa cat cat cca caa aaa caa caa	263
His Glu Gln Gln His His Pro Gln Gln His His Pro Gln Lys Gln Gln	
35 40 45	
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His Gln Pro Pro Pro Gln His His Gln Gln Gln Gln His Gln Gln Gln	
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caa gtt cac atg caa cca caa aaa cat cag caa caa caa gaa gtt cat	359
Gln Val His Met Gln Pro Gln Lys His Gln Gln Gln Gln Glu Val His	
65 70 75 80	
ggt caa caa caa caa caa caa ccg cag cac caa caa caa caa caa caa	407
Val Gln Gln Gln Gln Gln Gln Pro Gln His Gln Gln Gln Gln Gln	

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Gln Gln Ser Gln Gly His Val	Gln Gln His Glu Gln Ser His Glu Gln		
115	120	125	
cac caa gga cag agc cat gag	caa caa cat caa caa caa ttc cag ggt		551
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cat gac aag cag caa caa cca	caa cag cct cag caa tat cag cag ggc		599
His Asp Lys Gln Gln Gln Pro	Gln Gln Pro Gln Gln Tyr Gln Gln Gly		
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Asn Cys His Glu Phe Leu Arg	Gln Gln Cys Ser Pro Leu Val Met Pro		
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Phe Leu Gln Ser Arg Leu Ile	Gln Pro Ser Ser Cys Gln Val Leu Gln		
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Gln Ala Ile Tyr Asn Met Val	Gln Ser Ile Ile Gln Glu Glu Gln Gln		
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Gly Gly Asn Leu Asp Ser Ser	Thr Ile Pro Thr Ile Asn Val Arg Leu		
275	280	285	
gta cca ctc ata cta cca aaa	taatccatgc agcagcaatg acattagtgg		1034
Val Pro Leu Ile Leu Pro Lys			
290	295		
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 His Gln Pro Pro Pro Gln His His Gln Gln Gln Gln His Gln Gln Gln  
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 130 135 140  
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 180 185 190  
 Asn Cys His Glu Phe Leu Arg Gln Gln Cys Ser Pro Leu Val Met Pro  
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aag atc gcc gcg gcg gcg gcg gcg gcg ctg tgc ttc gcg gcc ctg gtg	164	
Lys Ile Ala Ala Ala Ala Ala Ala Ala Leu Cys Phe Ala Ala Leu Val		
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gcc gtg gcc gtc tgc caa ggc gag gtc gag cgg cag agg ctc agg gac	212	
Ala Val Ala Val Cys Gln Gly Glu Val Glu Arg Gln Arg Leu Arg Asp		
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ctg cag tgc tgg cag gag gtc cag gag agc ccg ctc gac gcg tgc cgc	260	
Leu Gln Cys Trp Gln Glu Val Gln Glu Ser Pro Leu Asp Ala Cys Arg		
	35	40 45 50
cag gtc ctc gac cgg cag cta acc ggc ggc ggc ggc ggc ggc ggc gtt	308	
Gln Val Leu Asp Arg Gln Leu Thr Gly Gly Gly Gly Gly Gly Gly Val		
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ggc ccg ttc cgg tgg ggc acc ggg ctc cgg atg cgg tgc tgc cag cag	356	
Gly Pro Phe Arg Trp Gly Thr Gly Leu Arg Met Arg Cys Cys Gln Gln		
	70	75 80
ctc cag gac gtg agc cgc gag tgc cgc tgc gcc gcc atc cgg agc atg	404	
Leu Gln Asp Val Ser Arg Glu Cys Arg Cys Ala Ala Ile Arg Ser Met		
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Val Arg Gly Tyr Glu Glu Ala Met Pro Pro Leu Glu Lys Gly Trp Trp		
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	135	140 145
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acc acc ggc ggc ggg cca agg atc ggc cgc gtg agg ctt acg aag gcc	644	
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	165	170 175
cgg gag tac gcc gcg ggg ttg ccg atg atg tgc cgg ctg tcg gag ccc	692	
Arg Glu Tyr Ala Ala Gly Leu Pro Met Met Cys Arg Leu Ser Glu Pro		
	180	185 190
cag gag tgc agc atc ttc tcc ggc ggc gac cag tac tagctacat	738	
Gln Glu Cys Ser Ile Phe Ser Gly Gly Asp Gln Tyr		

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 cagaatgacg tagctctgac gtgggctcgc aatattgtcg cgtgttcggt acaataatga 858  
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 35 40 45  
 Cys Arg Gln Val Leu Asp Arg Gln Leu Thr Gly Gly Gly Gly Gly Gly  
 50 55 60  
 Gly Val Gly Pro Phe Arg Trp Gly Thr Gly Leu Arg Met Arg Cys Cys  
 65 70 75 80  
 Gln Gln Leu Gln Asp Val Ser Arg Glu Cys Arg Cys Ala Ala Ile Arg  
 85 90 95  
 Ser Met Val Arg Gly Tyr Glu Glu Ala Met Pro Pro Leu Glu Lys Gly  
 100 105 110  
 Trp Trp Pro Trp Gly Arg Gln Gln Gln Pro Pro Pro Gln Gly Gly Gly  
 115 120 125  
 Gly Gly Gln Gly Gly Tyr Tyr Tyr Pro Cys Ser Arg Pro Gly Glu Gly  
 130 135 140  
 Tyr Gly Tyr Gly Gln Gly Gly Gln Arg Gln Met Tyr Pro Pro Cys Arg  
 145 150 155 160  
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ctg	ctc	ctc	ctc	ctg	tgc	tgc	tcc	ggc	acc	tcg	tgg	gga	tgg	agc	acg	150
Leu	Leu	Leu	Leu	Leu	Cys	Cys	Ser	Gly	Thr	Ser	Trp	Gly	Trp	Ser	Thr	
	25					30				35						
tcc	cgg	gga	gga	gcc	gcc	agg	gag	tgc	ggc	ttc	gat	ggc	aag	ctg	gag	198
Ser	Arg	Gly	Gly	Ala	Ala	Arg	Glu	Cys	Gly	Phe	Asp	Gly	Lys	Leu	Glu	
40					45				50					55		
gcc	ctg	gag	ccg	cgc	cac	aag	gtg	cag	tct	gag	gcc	ggc	tcc	gtc	cag	246
Ala	Leu	Glu	Pro	Arg	His	Lys	Val	Gln	Ser	Glu	Ala	Gly	Ser	Val	Gln	
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Tyr	Phe	Ser	Arg	Phe	Asn	Glu	Ala	Asp	Arg	Glu	Leu	Thr	Cys	Ala	Gly	
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atc	ttc	gcc	gtc	cgc	gtc	gtc	gtc	gac	gcc	atg	ggc	ctc	ctg	ctc	cct	342
Ile	Phe	Ala	Val	Arg	Val	Val	Val	Asp	Ala	Met	Gly	Leu	Leu	Leu	Pro	
	90					95						100				
cga	tac	tcc	aac	gtc	cat	tcg	ctt	gtc	tac	atc	gtc	caa	ggg	aga	ggg	390
Arg	Tyr	Ser	Asn	Val	His	Ser	Leu	Val	Tyr	Ile	Val	Gln	Gly	Arg	Gly	
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Ile	Ile	Gly	Phe	Ser	Phe	Pro	Gly	Cys	Gln	Glu	Glu	Thr	Gln	Gln	Gln	
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Gln	Tyr	Gly	Tyr	Gly	Tyr	Gly	Tyr	Gly	His	His	His	His	Gln	His	Asp	
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cac	cac	aag	atc	cac	cga	ttc	gag	cag	ggc	gac	gtg	gtg	gcc	atg	ccg	534
His	His	Lys	Ile	His	Arg	Phe	Glu	Gln	Gly	Asp	Val	Val	Ala	Met	Pro	
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gcc	ggc	gcc	cag	cac	tgg	ctg	tac	aac	gac	ggc	gac	gcg	ccg	ctt	gtg	582
Ala	Gly	Ala	Gln	His	Trp	Leu	Tyr	Asn	Asp	Gly	Asp	Ala	Pro	Leu	Val	
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	185					190					195					
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Ser	Met	Arg	Lys	Phe	Leu	Leu	Ala	Gly	Gly	Phe	Ser	Lys	Gly	Gln	Pro	
200					205				210					215		
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His	Phe	Ala	Glu	Asn	Ile	Phe	Lys	Gly	Ile	Asp	Ala	Arg	Phe	Leu	Ser	
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Glu Ala Leu Gly Val Ser Met His Val Ala Glu Lys Leu Gln Ser Arg	
235 240 245	
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Arg Asp Gln Arg Gly Glu Ile Val Arg Val Glu Pro Glu His Gly Phe	
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His Gln Leu Asn Pro Ser Pro Ser Ser Ser Ser Phe Ser Phe Pro Ser	
265 270 275	
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Ser Gln Val Gln Tyr Gln Thr Cys Gln Arg Asp Val Asp Arg His Asn	
280 285 290 295	
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Asp Val Tyr Ser Pro Gly Ala Gly Arg Ile Thr Arg Leu Thr Ser His	
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Lys Phe Pro Val Leu Asn Leu Val Gln Met Ser Ala Val Arg Val Asp	
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Leu Tyr Gln Asp Ala Ile Met Ser Pro Phe Trp Asn Phe Asn Ala His	
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agc gcc atg tac ggc atc agg ggc agt gca agg gtc cag gtc gcc agc	1158
Ser Ala Met Tyr Gly Ile Arg Gly Ser Ala Arg Val Gln Val Ala Ser	
360 365 370 375	
gac aac ggg acc acg gtg ttc gac gac gtg ctc cgt gcg ggg cag ctg	1206
Asp Asn Gly Thr Val Phe Asp Asp Val Leu Arg Ala Gly Gln Leu	
380 385 390	
ctc atc gta ccc cag ggc tac ctc gtc gcc acc aag gcg cag gga gaa	1254
Leu Ile Val Pro Gln Gly Tyr Leu Val Ala Thr Lys Ala Gln Gly Glu	
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ggc ttc cag tac atc gcc ttc gag acg aac cct gac acc atg gtc agc	1302
Gly Phe Gln Tyr Ile Ala Phe Glu Thr Asn Pro Asp Thr Met Val Ser	
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His Val Ala Gly Lys Asn Ser Val Leu Ser Asp Leu Pro Ala Ala Val	
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Ile Ala Ser Ser Tyr Ala Ile Ser Met Glu Glu Ala Ala Glu Leu Lys	
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Asn Gly Arg Lys His Glu Leu Ala Val Leu Thr Pro Ala Gly Ser Gly  
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Thr	Ser	Trp	Gly	Trp	Ser	Thr	Ser	Arg	Gly	Gly	Ala	Ala	Arg	Glu	Cys
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Arg	Glu	Leu	Thr	Cys	Ala	Gly	Ile	Phe	Ala	Val	Arg	Val	Val	Val	Asp
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	130					135						140			
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Gly	Asp	Val	Val	Ala	Met	Pro	Ala	Gly	Ala	Gln	His	Trp	Leu	Tyr	Asn
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Val	Glu	Pro	Glu	His	Gly	Phe	His	Gln	Leu	Asn	Pro	Ser	Pro	Ser	Ser
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Ser	Ser	Phe	Ser	Phe	Pro	Ser	Ser	Gln	Val	Gln	Tyr	Gln	Thr	Cys	Gln
		275					280					285			
Arg	Asp	Val	Asp	Arg	His	Asn	Val	Cys	Ala	Met	Glu	Val	Arg	His	Ser
	290					295					300				



Val Glu Arg Leu Asp Gln Ala Asp Val Tyr Ser Pro Gly Ala Gly Arg  
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 Ile Thr Arg Leu Thr Ser His Lys Phe Pro Val Leu Asn Leu Val Gln  
 325 330 335  
 Met Ser Ala Val Arg Val Asp Leu Tyr Gln Asp Ala Ile Met Ser Pro  
 340 345 350  
 Phe Trp Asn Phe Asn Ala His Ser Ala Met Tyr Gly Ile Arg Gly Ser  
 355 360 365  
 Ala Arg Val Gln Val Ala Ser Asp Asn Gly Thr Thr Val Phe Asp Asp  
 370 375 380  
 Val Leu Arg Ala Gly Gln Leu Leu Ile Val Pro Gln Gly Tyr Leu Val  
 385 390 395 400  
 Ala Thr Lys Ala Gln Gly Glu Gly Phe Gln Tyr Ile Ala Phe Glu Thr  
 405 410 415  
 Asn Pro Asp Thr Met Val Ser His Val Ala Gly Lys Asn Ser Val Leu  
 420 425 430  
 Ser Asp Leu Pro Ala Ala Val Ile Ala Ser Ser Tyr Ala Ile Ser Met  
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 Glu Glu Ala Ala Glu Leu Lys Asn Gly Arg Lys His Glu Leu Ala Val  
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 Ala Gln Gln

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 acaacagcac caacaacaac atcaatgtga aggccaacaa caacatcacc aacaatcaca 180  
 aggccatgtg caacaacacg aacagagcca tgagcaacac caaggacaga gccatgagca 240  
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 <212> DNA  
 <213> Zea mays

<220>  
 <221> allele  
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 <223> 18 kD alpha-globulin, B73, partial

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 <211> 537  
 <212> DNA  
 <213> Zea mays

<220>  
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